DEOXYRIBONUCLEIC ACID PROFILING

Overview

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Introduction

The forensic biologist has traditionally used a large set of markers including blood group antigens and serum proteins to establish links between evidence and comparison samples. These markers are polymorphic and genetically determined. In 1985, a new technique was introduced which opened the door to the forensic use of deoxyribonucleic acid (DNA) technology: its inventor coined the term 'DNA fingerprinting'. Since then, DNA typing in this and many other forms has flourished and the forensic biologist now has access to a large variety of powerful techniques.

DNA and its Polymorphism

DNA is an extremely large linear molecule which stores genetic information in the form of a sequence of its constituent elements: the nucleotides. The DNA molecule is made up of two complementary chains or strands of nucleotides (**Figure 1**). There are four different nucleotides (symbolized by the letters A, C, T, G) whose chemical affinity determines the complementarity of the nucleotide sequences of the two strands of the DNA molecule. Nucleotides A and T, and G and C always face each other; as a consequence, the length of DNA fragments is usually expressed in 'base pair' (bp) units. This chemical affinity allows single strands of complementary DNA to hybridize to each other. Nucleotide chains are oriented, having so called 5′ and 3′ ends, and the two strands of DNA have an opposite orientation. The DNA synthesis occurs in the direction $5' \rightarrow 3'$.

The polymorphism within DNA resides partly in the existence of minor nucleotide sequence variations among different individuals at various locations (loci) in the DNA molecule, which has its counterpart in the polymorphism of the amino acid sequence of the proteins. The gene variants (the alleles) differ in their sequence. However, a more extensive and DNA-specific polymorphism exists in the noncoding DNA: the tandemly repeated sequences. These polymorphic loci are DNA fragments, made up of a nucleotide sequence (the repeat unit), tandemly repeated like a series of identical beads on a necklace (Figure 1). The repeat unit can be from two to more than 100 nucleotides long. The polymorphism comes from the extreme variation in the number of repeats. The alleles differ then by their size (length polymorphism). This kind of repetitive sequence has been called minisatellites or also variable number tandem repeat (VNTR). There is a huge reservoir of polymorphism in these sequences and it is their potential use which has stimulated the development of the various DNA typing procedures.

DNA Typing Procedures

Any biological material containing DNA may be useful, including blood, sperm, saliva, hair, autopsy tissue, bone. All DNA typing procedures involve a DNA isolation step, which allows the elimination of substances such as proteins which can interfere in the sometimes delicate enzymatic steps involved in any DNA typing method.

The traditional way to prepare samples is to dissolve them in a sodium dodecylsulfate (SDS) proteinase K solution which lyses the cells and digests the proteins. The samples are then extracted with a phenol/chloroform mixture and the DNA is finally ethanol-precipitated and dissolved in the adequate buffer. Polymerase chain reaction (PCR) analysis requires minimal amounts of DNA so that it is possible to start with samples so small that they are unlikely to contain substantial amounts of interfering molecules. Simple boiling of the samples in the presence of a heavy-metal chelator (Chelex resin) is then usually sufficient as a preparation method.

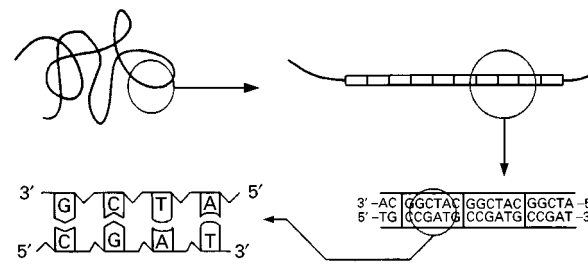

Figure 1 Schematic description at four increasing levels of magnification for DNA and VNTRs.

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Restriction Fragment Length Polymorphism (RFLP) Typing

The isolated DNA is reproducively cut into fragments by the action of a sequence specific DNA cutting enzyme, a restriction enzyme (hence RFLP). The fragments, which can be more than 20 000 bp long, are then separated according to their sizes by electrophoresis on agarose gel. The DNA fragments are transferred to a nylon membrane to which they will remain attached but are still accessible for hybridization with a probe. This membrane will provide a replica of the electrophoresis product. Labelled pieces of DNA having a sequence complementary to the repetitive sequence to be detected (the probe) are added to the nylon membrane and hybridize to the appropriate DNA fragments. These can finally be detected by autoradiography with a film sensitive to the labelled probe (**Figure 2**). The DNA fragments to be detected will appear on the film as dark bands (**Figures 2** and **3**). Their position will be a measure of their size, which is itself proportional to the number of repetitive elements in the VNTR. A comparison with DNA fragments of known sizes allows an accurate size determination. This first probe can be stripped from the membrane allowing for reprobing with a second probe, etc. There is a large choice of VNTRs available for RFLP typing (**Table 1**). It is the same for restriction enzymes: but a few have found wider use because of their robustness and their ability to cut DNA into small fragments. These enzymes are Hae III, Hinf I, Pst I, Alu I and Pvu II, the first two being the most used. The labelling of the probe is traditionally done through the use of ^{32}P-labelled nucleotides. However, probes coupled to enzymes catalysing the production of a chemiluminescent substance allow detection limits as low as those obtained by radioactive means.

The probe can be designed so as to detect a single VNTR locus; it is then a single locus probe (SLP). If the individual has inherited DNA from his parents with a different number of repeats at the analysed VNTR, the result is in the form of two bands (heterozygote); otherwise, there will be a single band (homozygote). But since the repeat units of different VNTRs often have sequence similarities to each other, it is possible to detect a whole family of VNTRs at the same time provided a probe is used under conditions allowing hybridization with partially complementary DNA fragments. In this case we speak of a multilocus probe (MLP) and the result appears in the form of a set of bands with a very individual pattern similar to a bar code.

Polymerase Chain Reaction (PCR)

The advent of the PCR has dramatically enlarged the spectrum of methods available for DNA typing. The PCR is a DNA amplification method which cyclically reproduces the natural DNA replication. Each cycle consists of (1) a denaturation step where the two DNA strands are separated by heating, (2) an annealing step where, after cooling, short synthetic DNA strands (the primers) are hybridized on both sides of the DNA fragment to be amplified, and (3) an elongation step where a DNA polymerase adds nucleotides to the primers to synthesize the DNA strands complementary to the template DNA. The result of many cycles is millions of copies of DNA fragment delimited by the primers. The use of a heat-stable polymerase has rendered the whole process very easy and allowed it to be automated. The nature of a PCR makes it naturally extremely sensitive, with a theoretical detection threshold of one molecule. The primers allow the amplification to be highly specific and the amplification product can then frequently be detected using a simple nonspecific detection method, which

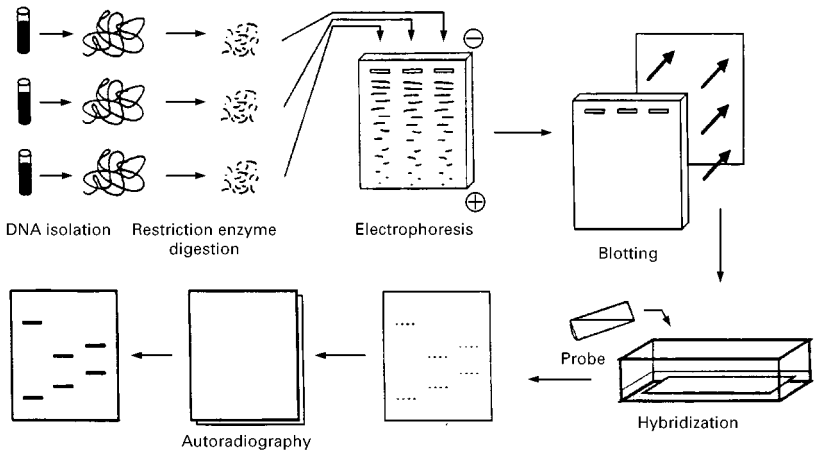

Figure 2 Schematic description of the main steps in RFLP typing.

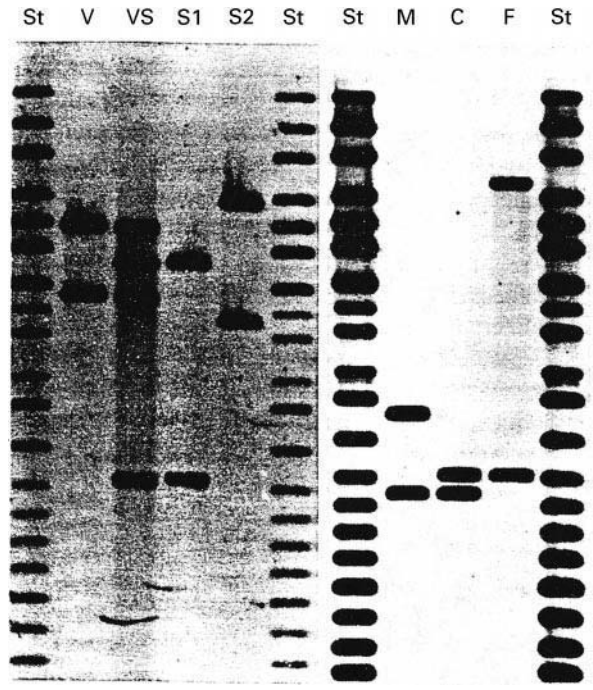

Figure 3 Typical examples of RFLP typing of forensic cases. On the left: sexual assault case; St, size markers, V, victim, VS, vaginal swab (containing material from the victim and her assailant), S1, suspect 1, S2, suspect 2. On the right: paternity test with M, mother, C, child, F, putative father.

makes the whole analytical process convenient and rapid.

PCR and Dot–Blot Analysis

Many methodologies have been designed which make use of the main principle of a PCR. In forensic science, PCR was first used to analyse sequence polymorphisms such as the polymorphism of the *HLA-DQα* locus. In that case, the alleles, which differ only by a few nucleotide changes, are identified after use of a PCR through hybridization with allele-specific probes, using a reverse dot–blot format (**Figure 4**): the various probes are attached to a membrane strip, arranged as a series of invisible dots to which the amplification products can hybridize depending upon thier sequence. Through the use of labelled nucleotides during the PCR, the genotype of the sample can be read through the appearance or not of coloured dots on the strip, at the position of each probe (Figure 4). In a way, the format is not very different from that of the strips for urine analysis so widely used in clinical medicine.

Amplification Fragment Length Polymorphism (AMP-FLP) Typing

Another use of a PCR has been the amplification of VNTRs to analyse their length polymorphism. However, the quite poor performance of PCRs in the amplification of large DNA fragments, such as those of the VNTR loci analysed through RFLP typing, has led to the search for smaller VNTRs (Table 1). By designing primers located on each side of a VNTR, it can be amplified by a PCR and the amplified fragments can be analysed by electrophoresis on agarose or polyacrylamide gels and compared to standards (Figure 4). While RFLP typing required the use of probes to detect specific VNTR-DNA fragments among thousands of other fragments, the amplification process here allows the use of nonspecific detection methods (ethidium bromide staining, silver staining) to make the bands visible. This kind of PCR-analysed VNTR polymorphism has been called amplification fragment length polymorphism (AMP-FLP).

Short Tandem Repeats (STR) Typing

The particularly high efficiency of PCR in the amplification of very small fragments has attracted attention toward a class of VNTRs made of very small repeats (di-, tri-, tetranucleotide repeats) (Table 1). They are sometimes called microsatellites

Table 1 Selection of some of the main DNA loci analysed by the various DNA typing methods

Locus	*Corresponding probe*	*Chromosome location*	*Repeat unit length (bp)*	*Typing method used*	*Heterozygosity[b] (%)*
—	33.6	1[a]	37[a]	multilocus RFLP	—
D1S7	*MS1*	1	9	monolocus RFLP	> 99
D7S21	*MS31*	7	20	monolocus RFLP	98
D2S44	*YNH24*	2	31	monolocus RFLP	94
D10S28	*TBQ7*	10	33	monolocus RFLP	97
HLA-DQα	—	6	—	PCR + dot blotting	79
D1S80	*MCT118*	1	16	AMP-FLP	80
D17S5	*YNZ22*	17	70	AMP-FLP	82
APOC2	*Mdf5*	19	2	STR	80
HUMTH01	—	11	4	STR	80

[a]These characteristics refer to the VNTR used as the multilocus probe.
[b]Heterozygosity is calculated here as the percentage of apparent heterozygotes in the population (Caucasian in this case).

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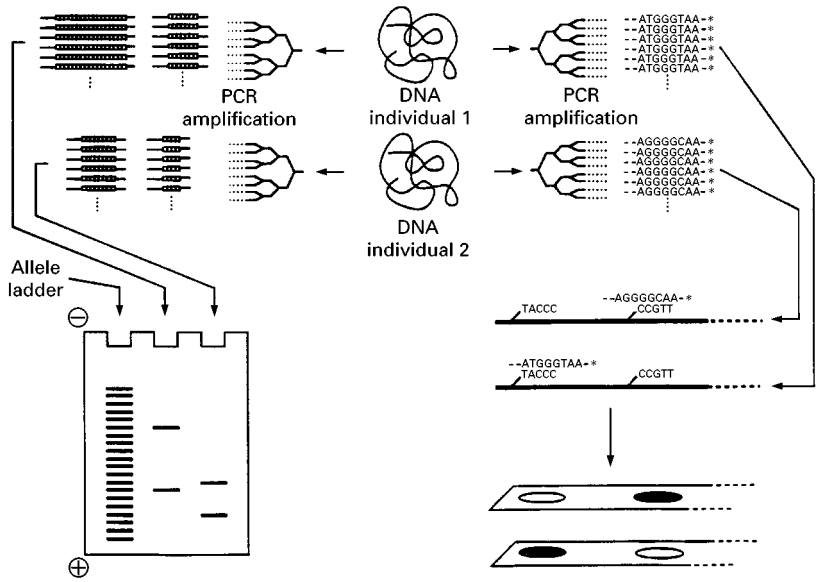

Figure 4 A PCR amplification for AMP-FLP typing (left) and reverse dot–blot analysis (right).

or short tandem repeats (STRs) and they are probably the richest class of polymorphic loci available. Their amplification conditions are simple and the size range of their alleles is usually narrow. They are then well suited to multiplexing: it is indeed easy to choose microsatellite loci and adequate primers so as to obtain amplified DNA fragments situated in well separated size ranges for each locus. Consequently a whole group of STRs can be amplified at the same time and analysed on the same gel. The small size of their repeat unit, however, is also a disadvantage. The various alleles only differ in length by two, three or four nucleotides. Such a separation power is only possible through the more complex technology of sequencing gel electrophoresis. However, the sequencing technology is undergoing constant improvement due to the challenge of the human genome sequencing project, and STR typing has benefited from the developments in that field such as fluorescent labelling and automatic sequencing.

Minisatellite Variant Repeat (MVR)-PCR

The polymerase chain reaction has made possible yet another powerful DNA typing method: MVR-PCR. This has been designed to reveal a polymorphism consisting of variations in the sequence of the repeat unit within some VNTRs. Instead of being a pure repetition of one repeat unit, some VNTRs are composed of combinations of two or more almost identical repeat units. It is easy to calculate that even with only two repeat variants a and b, the number of possible combinations of repeats is huge. The sequence of repeats is revealed through a process somehat similar to the Sanger DNA sequencing method (**Figure 5**). The PCR is carried out in parallel in two tubes in a mixture containing a primer complementary to a DNA sequence outside the VNTR and a low concentration of primer complementary to the repeat unit variant a. This set of two primers allows the multiplication of an array of all the possible fragment going from one end of the VNTR to every repeat a. In the second tube, the use of a primer complementary to the repeat unit variant b allows the multiplication of another array of all the possible fragments going from one end of the VNTR to every repeat b. An unequal amplification of the short versus long fragments is avoided through the use of a tag attached to the two alternative primers. This tag is a short strand of DNA. A fourth primer complementary to this tag is then used to allow the further amplification of the arrays of fragments. The content of the two tubes is then loaded on two adjacent lanes of an agarose gel. After electrophoresis, Southern blotting, hybridization with a probe for the VNTR and autoradiography, the result appears in the form of two parallel ladders of bands with fainter or missing rungs. For an individual, the result is indeed the sum of the results given by two VNTR fragments, those inherited from the mother and the father: at each repeat position in the VNTR the subject can have variant a twice, variant b twice, or a once and b once. These three possibilities can easily be coded by the numbers 1, 2, 3, allowing a simple digitization of the result (Figure 5). It is clear that the existence of more than two repeat variants makes the coding more complex and the system more informative but the principle remains the same. With MVR-PCR, there is no need to have carefully standardized electrophoretic conditions. Each

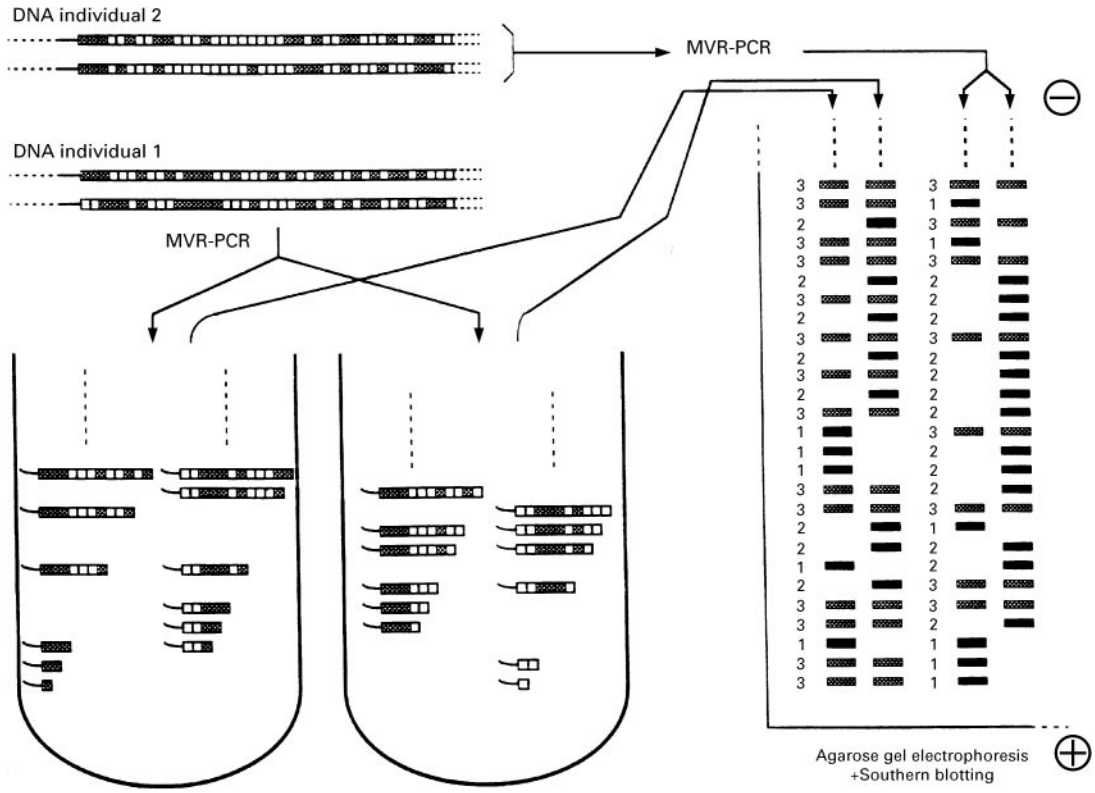

Figure 5 Schematic description of MVR-PCR.

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result is literally read by itself, and different samples are simply compared at the level of their codes.

Other Methods

Other DNA typing methods have been developed or proposed, and still others are yet to appear. Two methods are worth mentioning. One is mitochondrial DNA (mtDNA) sequence analysis. A DNA sequence analysis after PCR amplification is a natural way to examine DNA polymorphism. However, because it is unable to reveal more than a few hundred base pairs at a time, and because of its complexity, it is not as attractive as the above-mentioned methods. However, it has been a precious tool in the analysis of mitochondrial DNA, which is a small piece of DNA, maternally inherited, present in all mitochondria. Part of it (the D-loop) contains a highly polymorphic sequence and its sequence determination is therefore very informative. Owing to the presence of more than 1000 copies in each cell. mtDNA analysis is very sensitive. Moreover, hair shafts, which do not contain nuclear DNA, are rich in mtDNA and are therefore amenable to genetic analysis.

The second method is polymorphic sequence-tagged sites (pSTS) analysis. This is a method designed to reveal single base pair changes. After a PCR amplification of the DNA fragment containing the polymorphic base pair, a ligation assay is performed using an antigen-labelled primer and one of two biotin-labelled primers each being specific for one of the two possible alleles. In the presence of the corresponding sample allele, the biotin-labelled primer is ligated to the antigen-labelled primer. After capture of the product in microtitre plates coated with streptavidin (a binding protein for biotin), the presence of the antigen can be detected using a traditional immunoenzymatic method (ELISA procedure). The combined analysis of more than 15 such two-allele sites can reveal genotypes with frequencies below 10^{-6}. The most interesting features of this method are its technical simplicity and its straightforward interpretation (positive or negative readout) which make it particularly amenable to automation. It could reach its highest performance if all the loci could be analysed simultaneously within the same tube.

Applications

Deoxyribonucleic acid typing gained prominence from the start because of its identification power. It is the most powerful identification technique after fingerprint examination. It represents a big jump from the traditional protein polymorphism analysis where powerful identification could only be reached by the

sequential analysis of more than 20 polymorphic systems, each requiring its own analytical process. The improvement is particularly evident in semen analysis where the number of available polymorphic systems was extremely low. In RFLP typing, the analysed VNTR loci are so polymorphic that most of the possible genotypes have frequencies below 1%. It is then easy to calculate that the combined analysis of four such loci reveals genotypes with frequencies of the order of 10^{-8}. Both AMP-FLP typing and STR typing use smaller, less polymorphic and therefore less informative VNTRs, but a similarly high information yield can be reached by increasing the number of loci analysed.

Interpretation

Forensic identification is achieved through the demonstration of matching biological characteristics between evidence and comparison material. The matching is straightforward when discrete and well-identifiable alleles are analysed such as in the various methods derived from a PCR. However, in RFLP typing, a match is not always easy to establish. First there is the intrinsic difficulty of having to deal with alleles which cannot each be differentiated by electrophoresis. Indeed, because of the size range of the DNA fragments, the separation power of electrophoresis is insufficient to separate alleles differing in length by only one repeat unit. Two samples having bands at an identical position may in fact possess different alleles. Secondly, there is the possibility that a DNA sample originating from the same person as the comparison sample contains interfering molecules, leading to a different electrophoretic behaviour and shifted band positions. This bandshifting can only be demonstrated and evaluated through the use of proper controls (internal standards).

The next step in the interpretation is the evaluation of the power of the evidence. It is usually expressed as a ratio of the probability of the evidence under the hypothesis that the evidential material has the same source as the comparison sample and the probability of the evidence under the hypothesis that somebody else is the source of the evidence material. This ratio is normally inversely proportional to the frequency of the genetic characteristics detected in the adequate reference populaton. The determination of these frequencies is a difficult task. The extreme variability of the VNTR loci makes the gathering of genotype frequency data unrealistic. Statistically trustworthy frequencies would require the analysis of a huge number of individuals. It is thus necessary to rely on allele frequencies to calculate the genotype frequencies by multiplication. The frequency of genotype A_1A_2 at locus A is the product $2a_1a_2$ (with a_1 and a_2 being the respective allele frequencies). The frequency of the combined genotypes at four loci is then $2a_1a_2 \times 2b_1b_2 \times 2c_1c_2 \times 2d_1d_2$. However, these multiplications can only be done under the assumption of statistical independence of the multiplied factors. This translates into certain assumptions related to the genetic independence of the analysed VNTR loci and to the genetic structure of the populations (Hardy-Weinberg equilibrium).

Controversy has arisen over the possibility of the existence of genetic substructuring within the populations. Some geneticists expressed concern that the frequency of a genotype A_1A_2 might have an apparent value using the general population database, but that the true frequency might be much higher owing to the high frequency of these specific alleles in a genetically distinct population subgroup. At the extreme, if alleles A_1A_2 only appear in this subpopulation where they have a frequency of 50% each, the detection of allele A_1 in a sample would make the detection of allele A_2 almost certain. Because of such effects, combined genotype frequencies could be underestimated by several orders of magnitude. The accumulating data suggest, however, that there is not much reason to worry about such effects. The VNTR loci are extremely polymorphic in every population studied and, for any given genotype constellation, there is an extremely low probability of having substantial frequency differences when calculating with one population data or another. Moreover, within the major races, the frequency distributions are very similar between different populations. And finally, forensic laboratories use very conservative approaches which always favour the accused at each interpretation step.

Paternity Testing

The identification power of DNA typing has naturally been used in paternity testing (Figure 3). But here the question relates to the transmission of genetic material from one generation to the other. Mutations which can cause apparent exclusions of true fathers then have to be taken into account. The polymorphism of the VNTRs is linked to an exceptionally high mutation rate. This mutation rate can be below 10^{-4} to more than 0.05 mutations, per meiosis for the most polymorphic loci such as *D1S7*. This has to be compared to the mutation rate of coding DNA sequences which is estimated to be around 10^{-5} for a 1000 bp gene. The calculation of probability of paternity has to integrate these mutation rates. But it remains true that the increased power of DNA typing has made paternity testing much easier and has allowed the solution of complex situations, such as the unavailability of the putative father, which sometimes remained unsolved with traditional typing.

Practical Use

In the real world of forensic science, there are practical contingencies which can be the source of difficulties or even interpretation errors. An important contingency is the quantity of the evidential material. Any living cell contains about 6 pg of DNA, and the main forensic DNA sources contain about 30 ng μL^{-1} (blood), 400 ng μL^{-1} (semen), 2 ng μL^{-1} (saliva) and 0–250 ng per hair root. As indicated in **Table 2**. RFLP typing would require at least a few microlitres of blood and the various PCR methods require about 0.05 μL. The theoretical PCR sensitivity of one molecule would suggest that less than 1 nL of blood should be sufficient. However, this does not take into account the potential loss during DNA isolation, or, more importantly, that one of the alleles may be absent or underepresented in small samples containing only a few molecules, for simple stochastic reasons. As a consequence, it will not appear at the end of the process: a heterozygote will appear as a homozygote. In other words, there may be an allele drop-out.

Another important factor is the quality of the material. Although DNA is a robust molecule and usable DNA fragments have been recovered from thousand year old mummified bodies, it can very quickly be degraded into smaller fragments when exposed to humidity, heat or sunlight. With such degraded samples, DNA typing methods like STR typing, which analyse very short DNA fragments, may still be applied successfully. However, RFLP typing may be no longer possible. Or even worse, a DNA sample possessing a large and a small allele at a VNTR locus may have larger fragments which are too degraded to be detected while the smaller ones will have survived enough to give a detectable band. Here again, the result is an allele drop-out. That is why, in the usual procedure, a small portion of the sample is loaded on a minielectrophoresis gel followed by nonspecific DNA staining. The examination of the intensity of the staining and the average size of the DNA fragments allows both quantitative and qualitative evaluation of the available DNA. The quality of the material can also affect RFLP typing through the inhibition of the restriction enzyme. One of the expected DNA fragments may appear at a position corresponding to a larger size than it should, because the enzyme has failed to cut the restriction site closest to the VNTR efficiently.

The experienced analyst usually has no problems avoiding interpretation errors arising from the abovementioned situations or others (extra bands due to unsufficiently stringent hybridization, incomplete stripping, internal restriction site or bacterial contamination, missing bands due to blotting problems, etc.). However, without extensive controls, it may be difficult to prove the tentative explanation. And the limited amount of evidence material usually precludes repeating an analysis.

With PCR-derived methods, there are a few specific potential sources of error worth mentioning. The first is contamination. A PCR is so senstitive that inadvertent transfer of DNA from one sample to another, from laboratory personnel to the samples, etc., can happen and be unnoticed. The large-scale use of negative controls should reveal any such contamination. Moreover, the establishment of adequate laboratory design and use of pertinent working guidelines and decontamination procedures should prevent the occurrence of such damaging episodes. The second source of error is differential amplification. The trustful amplification of a heterozygote requires that the two alleles are amplified with the same efficiency, otherwise the result is an allele drop-out. Consequently, the conditions which lead to such differential amplification have to be established and the proper precautions must be taken.

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Table 2 Main characteristics of the various techniques available for DNA typing

	Amount of genomic DNA required	*Ability to use damaged DNA*	*Probability of matching per locus analysed*[a]	*Degree of automation possible*
RFLP typing with single locus probes	> 20 ng	−	< 1%	−
RFLP typing with multilocus probes	> 500 ng	−	$< 10^{-7}$[b]	−
PCR + dot–blot analysis (*HLA-DQα* typing)	< 1 ng	+ +	7%	+
AMP-FLP typing	< 1 ng	+ +	5–10%	+ +
STR typing	< 1 ng	+ + +	2–10%	+ + +
MVR-PCR	> 1 ng	+	$< 10^{-6}$[c]	+
mtDNA sequencing	≪ 1 ng	+ +	10^{-4}[c]	+ +
pSTS analysis	< 1 ng	+ + +	40%	+ + + +

[a]The probability of matching (*Pm*) is the probability that two individuals taken at random have the same genotype. $Pm = \sum_{i=1}^{n} P_i^2$ where P_i is the frequency of the genotype for the analysed locus.
[b]*Pm* is that for the whole set of loci detected by this probe.
[c]These numbers are estimates based on limited population samples.

The potent identification power of DNA typing makes the establishment of databases for the storage of DNA profiles possible and desirable. New profiles can be compared with stored profiles to identify criminals, link unsolved cases, etc. This necessitates a high level of standardization among the laboratories participating in the information exchange networks. They must at least analyse the same polymorphic loci and, for RFLP typing, they must use the same enzymes and similar analytical protocols. Because of the large choice of polymorphic loci and analytical methods, the minimum degree of coherence is not at all warranted unless a strong effort is made between the laboratories to reach a consensus. And a consensus is difficult to reach in a fast moving field where new technologies are constantly being developed.

There is no doubt that DNA typing is the 'safest' identification technique ever used in forensic biology. But, because of its power and its consequent impact in a courtroom, it is and will remain under intense scrutiny by the forensic and legal communities. Consequently, a lot of attention has been paid to quality control and proficiency testing. There is certainly the opportunity for future improvements and developments in this field.

See Colour Plate 75.

See also: **II/Electrophoresis:** Blotting; Deoxyribonucleic Acid, Theory of Techniques for Separation; One-dimensional Polyacrylamide Gel Electrophoresis; One-dimensional Sodium Dodecyl Sulphate Polyacrylamide Gel Electrophoresis.

Further Reading

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Capillary Electrophoresis

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Introduction

One of the earliest reports on DNA capillary electrophoresis (CE) was by Cohen *et al*. who demonstrated the high resolution of nucleosides and oligonucleotides, in the absence of a sieving gel, by simply trapping the analyte into sodium dodecyl sulfate (SDS) micelles. One year later, in 1988, the same author discussed the separation of DNA restriction fragments in a gel-free environment. The first reports on the use of polyacrylamide gel capillary columns to separate DNA with remarkable efficiency and resolution were presented the same year by Guttman *et al*. and Cohen *et al*. By 1989, gel-filled CE was already a well-established technique. These preliminary reports were then followed by a flurry of articles describing applications of capillary gel electrophoresis (CGE) to the separation of DNA restriction fragments. In spite of the high resolving power and efficiency offered by CGE in the analysis of nucleic acids (15–30 million plates per metre and a single-base resolution for fragments ranging from 15 to more than 500 bases were reported), the difficulties of producing adequate gel-filled capillaries hindered their greater application. Heiger *et al*. proposed, as early as 1990, the use of polyacrylamide cross-linked with a very low or zero concentration of *N*,*N*-methylenebisacrylamide. Strangely enough, the revolution brought about by the use of polymer solutions as sieving matrices was only evident in 1991 as a result of the work of Guttman and Cooke and Grossman and Soane. Since then, hundreds of reports have demonstrated the advantages of performing DNA separations in a narrow fused silica capillary. Due to its high resolving power and quantitative capability, CE has been successfully applied to different kinds of DNA analysis, including the following: DNA sequencing, separation of restriction fragments, polymerase chain reaction (PCR) products and synthetic oligonucleotides.

Advantages of Capillary over Slab Gel Electrophoresis

For many years electrophoretic separations of DNA were carried out in slab gels. One of the main